P. Mertz

ENTERED

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            RAW SEQUENCE LISTING              DATE: 08/07/2001
            PATENT APPLICATION:  US/09/521,195   TIME: 13:22:26

            Input Set : A:\06501-057001.txt
            Output Set: N:\CRF3\08072001\I521195.raw


  3 <110> APPLICANT: Nezu, Jun-Ichi
  4        Oku, Asuka
  6 <120> TITLE OF INVENTION: TRANSPORTER GENES
  8 <130> FILE REFERENCE: 06501-057001
 10 <140> CURRENT APPLICATION NUMBER: 09/521,195
 11 <141> CURRENT FILING DATE: 2000-03-07
 13 <150> PRIOR APPLICATION NUMBER: JP 10/156660
 14 <151> PRIOR FILING DATE: 1998-05-20
 16 <150> PRIOR APPLICATION NUMBER: JP 9/260972
 17 <151> PRIOR FILING DATE: 1997-09-08
 19 <150> PRIOR APPLICATION NUMBER: PCT/JP98/04009
 20 <151> PRIOR FILING DATE: 1998-09-07
 22 <160> NUMBER OF SEQ ID NOS: 32
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 551
 26 <212> TYPE: PRT
 27 <213> ORGANISM: Homo sapiens
 29 <400> SEQUENCE: 1
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 33            20                  25                  30
 34 Gly Phe Asn Gly Met Ser Val Val Phe Leu Ala Gly Thr Pro Glu His
 35            35                  40                  45
 36 Arg Cys Arg Val Pro Asp Ala Ala Asn Leu Ser Ser Ala Trp Arg Asn
 37     50                  55                  60
 38 Asn Ser Val Pro Leu Arg Leu Arg Asp Gly Arg Glu Val Pro His Ser
 39 65                  70                  75                  80
 40 Cys Ser Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Ala Leu Gly
 41             85                  90                  95
 42 Leu Glu Pro Gly Arg Asp Val Asp Leu Gly Gln Leu Glu Gln Glu Ser
 43            100                 105                 110
 44 Cys Leu Asp Gly Trp Glu Phe Ser Gln Asp Val Tyr Leu Ser Thr Val
 45            115                 120                 125
 46 Val Thr Glu Trp Asn Leu Val Cys Glu Asp Asn Trp Lys Val Pro Leu
 47     130                 135                 140
 48 Thr Thr Ser Leu Phe Phe Val Gly Val Leu Leu Gly Ser Phe Val Ser
 49 145                 150                 155                 160
 50 Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Asn Val Leu Phe Ala Thr
 51            165                 170                 175
 52 Met Ala Val Gln Thr Gly Phe Ser Phe Leu Gln Ile Phe Ser Ile Ser
 53            180                 185                 190
 54 Trp Glu Met Phe Thr Val Leu Phe Val Ile Val Gly Met Gly Gln Ile
 55            195                 200                 205
 56 Ser Asn Tyr Val Val Ala Phe Ile Leu Gly Thr Glu Ile Leu Gly Lys
 57     210                 215                 220
 58 Ser Val Arg Ile Ile Phe Ser Thr Leu Gly Val Cys Thr Phe Phe Ala
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59 225                     230                235                240
60 Val Gly Tyr Met Leu Leu Pro Leu Phe Ala Tyr Phe Ile Arg Asp Trp
61                 245                 250                255
62 Arg Met Leu Leu Leu Ala Leu Thr Val Pro Gly Val Leu Cys Val Pro
63                 260                 265                270
64 Leu Trp Trp Phe Ile Pro Glu Ser Pro Arg Trp Leu Ile Ser Gln Arg
65                 275                 280                285
66 Arg Phe Arg Glu Ala Glu Asp Ile Ile Gln Lys Ala Ala Lys Met Asn
67         290                 295                 300
68 Asn Thr Ala Val Pro Ala Val Ile Phe Asp Ser Val Glu Glu Leu Asn
69 305                 310                 315                320
70 Pro Leu Lys Gln Gln Lys Ala Phe Ile Leu Asp Leu Phe Arg Thr Arg
71                 325                 330                335
72 Asn Ile Ala Ile Met Thr Ile Met Ser Leu Leu Leu Trp Met Leu Thr
73                 340                 345                350
74 Ser Val Gly Tyr Phe Ala Leu Ser Leu Asp Ala Pro Asn Leu His Gly
75                 355                 360                365
76 Asp Ala Tyr Leu Asn Cys Phe Leu Ser Ala Leu Ile Glu Ile Pro Ala
77         370                 375                 380
78 Tyr Ile Thr Ala Trp Leu Leu Leu Arg Thr Leu Pro Arg Arg Tyr Ile
79 385                 390                 395                400
80 Ile Ala Ala Val Leu Phe Trp Gly Gly Gly Val Leu Leu Phe Ile Gln
81                 405                 410                415
82 Leu Val Pro Val Asp Tyr Tyr Phe Leu Ser Ile Gly Leu Val Met Leu
83                 420                 425                430
84 Gly Lys Phe Gly Ile Thr Ser Ala Phe Ser Met Leu Tyr Val Phe Thr
85                 435                 440                445
86 Ala Glu Leu Tyr Pro Thr Leu Val Arg Asn Met Ala Val Gly Val Thr
87         450                 455                 460
88 Ser Thr Ala Ser Arg Val Gly Ser Ile Ile Ala Pro Tyr Phe Val Tyr
89 465         .         470                 475                480
90 Leu Gly Ala Tyr Asn Arg Met Leu Pro Tyr Ile Val Met Gly Ser Leu
91                 485                 490                495
92 Thr Val Leu Ile Gly Ile Phe Thr Leu Phe Phe Pro Glu Ser Leu Gly
93                 500                 505                510
94 Met Thr Leu Pro Glu Thr Leu Glu Gln Met Gln Lys Val Lys Trp Phe
95         515                 520                 525
96 Arg Ser Gly Lys Lys Thr Arg Asp Ser Met Glu Thr Glu Glu Asn Pro
97         530                 535                 540
98 Lys Val Leu Ile Thr Ala Phe
99 545                 550
101 <210> SEQ ID NO: 2
102 <211> LENGTH: 2135
103 <212> TYPE: DNA
104 <213> ORGANISM: Homo sapiens
106 <220> FEATURE:
107 <221> NAME/KEY: CDS
108 <222> LOCATION: (147)..(1799)
110 <400> SEQUENCE: 2
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RAW SEQUENCE LISTING   DATE: 08/07/2001
PATENT APPLICATION: US/09/521,195   TIME: 13:22:26

Input Set : A:\06501-057001.txt
Output Set: N:\CRF3\08072001\I521195.raw

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111 ccccggcttc gcgccccaat ttctaacagc ctgcctgtcc cccgggaacg ttctaacatc         60
113 cttggggagc gccccagcta caagacactg tcctgagaac gctgtcatca cccgtagttg        120
115 caagtttcgg agcggcagtg ggaagc atg cgg gac tac gac gag gtg atc gcc         173
116                                Met Arg Asp Tyr Asp Glu Val Ile Ala
117                                 1               5
119 ttc ctg ggc gag tgg ggg ccc ttc cag cgc ctc atc ttc ttc ctg ctc         221
120 Phe Leu Gly Glu Trp Gly Pro Phe Gln Arg Leu Ile Phe Phe Leu Leu
121 10                  15                  20                  25
123 agc gcc agc atc atc ccc aat ggc ttc aat ggt atg tca gtc gtg ttc         269
124 Ser Ala Ser Ile Ile Pro Asn Gly Phe Asn Gly Met Ser Val Val Phe
125                 30                  35                  40
127 ctg gcg ggg acc ccg gag cac cgc tgt cga gtg ccg gac gcc gcg aac         317
128 Leu Ala Gly Thr Pro Glu His Arg Cys Arg Val Pro Asp Ala Ala Asn
129             45                  50                  55
131 ctg agc agc gcc tgg cgc aac aac agt gtc ccg ctg cgg ctg cgg gac         365
132 Leu Ser Ser Ala Trp Arg Asn Asn Ser Val Pro Leu Arg Leu Arg Asp
133         60                  65                  70
135 ggc cgc gag gtg ccc cac agc tgc agc cgc tac cgg ctc gcc acc atc         413
136 Gly Arg Glu Val Pro His Ser Cys Ser Arg Tyr Arg Leu Ala Thr Ile
137     75                  80                  85
139 gcc aac ttc tcg gcg ctc ggg ctg gag ccg ggg cgc gac gtg gac ctg         461
140 Ala Asn Phe Ser Ala Leu Gly Leu Glu Pro Gly Arg Asp Val Asp Leu
141 90                  95                  100                 105
143 ggg cag ctg gag cag gag agc tgc ctg gat ggc tgg gag ttc agc cag         509
144 Gly Gln Leu Glu Gln Glu Ser Cys Leu Asp Gly Trp Glu Phe Ser Gln
145                 110                 115                 120
147 gac gtc tac ctg tcc acc gtc gtg acc gag tgg aat ctg gtg tgt gag         557
148 Asp Val Tyr Leu Ser Thr Val Val Thr Glu Trp Asn Leu Val Cys Glu
149                 125                 130                 135
151 gac aac tgg aag gtg ccc ctc acc acc tcc ctg ttc ttc gta ggc gtg         605
152 Asp Asn Trp Lys Val Pro Leu Thr Thr Ser Leu Phe Phe Val Gly Val
153         140                 145                 150
155 ctc ctc ggc tcc ttc gtg tcc ggg cag ctg tca gac agg ttt ggc agg         653
156 Leu Leu Gly Ser Phe Val Ser Gly Gln Leu Ser Asp Arg Phe Gly Arg
157     155                 160                 165
159 aag aac gtt ctc ttc gca acc atg gct gta cag act ggc ttc agc ttc         701
160 Lys Asn Val Leu Phe Ala Thr Met Ala Val Gln Thr Gly Phe Ser Phe
161 170                 175                 180                 185
163 ctg cag att ttc tcc atc agc tgg gag atg ttc act gtg tta ttt gtc         749
164 Leu Gln Ile Phe Ser Ile Ser Trp Glu Met Phe Thr Val Leu Phe Val
165                 190                 195                 200
167 atc gtg ggc atg ggc cag atc tcc aac tat gtg gta gcc ttc ata cta         797
168 Ile Val Gly Met Gly Gln Ile Ser Asn Tyr Val Val Ala Phe Ile Leu
169                 205                 210                 215
171 gga aca gaa att ctt ggc aag tca gtt cgt att ata ttc tct aca tta         845
172 Gly Thr Glu Ile Leu Gly Lys Ser Val Arg Ile Ile Phe Ser Thr Leu
173                 220                 225                 230
175 gga gtg tgc aca ttt ttt gca gtt ggc tat atg ctg ctg cca ctg ttt         893
176 Gly Val Cys Thr Phe Phe Ala Val Gly Tyr Met Leu Leu Pro Leu Phe
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177      235                   240                   245
179 gct tac ttc atc aga gac tgg cgg atg ctg ctg ctg gcg ctg acg gtg     941
180 Ala Tyr Phe Ile Arg Asp Trp Arg Met Leu Leu Leu Ala Leu Thr Val
181 250                   255                   260                   265
183 ccg gga gtg ctg tgt gtc ccg ctg tgg tgg ttc att cct gaa tct ccc     989
184 Pro Gly Val Leu Cys Val Pro Leu Trp Trp Phe Ile Pro Glu Ser Pro
185                   270                   275                   280
187 cga tgg ctg ata tcc cag aga aga ttt aga gag gct gaa gat atc atc     1037
188 Arg Trp Leu Ile Ser Gln Arg Arg Phe Arg Glu Ala Glu Asp Ile Ile
189                   285                   290                   295
191 caa aaa gct gca aaa atg aac aac aca gct gta cca gca gtg ata ttt     1085
192 Gln Lys Ala Ala Lys Met Asn Asn Thr Ala Val Pro Ala Val Ile Phe
193         300                   305                   310
195 gat tct gtg gag gag cta aat ccc ctg aag cag cag aaa gct ttc att     1133
196 Asp Ser Val Glu Glu Leu Asn Pro Leu Lys Gln Gln Lys Ala Phe Ile
197         315                   320                   325
199 ctg gac ctg ttc agg act cgg aat att gcc ata atg acc att atg tct     1181
200 Leu Asp Leu Phe Arg Thr Arg Asn Ile Ala Ile Met Thr Ile Met Ser
201 330                   335                   340                   345
203 ttg ctg cta tgg atg ctg acc tca gtg ggt tac ttt gct ctg tct ctg     1229
204 Leu Leu Leu Trp Met Leu Thr Ser Val Gly Tyr Phe Ala Leu Ser Leu
205                   350                   355                   360
207 gat gct cct aat tta cat gga gat gcc tac ctg aac tgt ttc ctc tct     1277
208 Asp Ala Pro Asn Leu His Gly Asp Ala Tyr Leu Asn Cys Phe Leu Ser
209                   365                   370                   375
211 gcc ttg att gaa att cca gct tac att aca gcc tgg ctg cta ttg cga     1325
212 Ala Leu Ile Glu Ile Pro Ala Tyr Ile Thr Ala Trp Leu Leu Leu Arg
213         380                   385                   390
215 acg ctg ccc agg cgt tat atc ata gct gca gta ctg ttc tgg gga gga     1373
216 Thr Leu Pro Arg Arg Tyr Ile Ile Ala Ala Val Leu Phe Trp Gly Gly
217         395                   400                   405
219 ggt gtg ctt ctc ttc att caa ctg gta cct gtg gat tat tac ttc tta     1421
220 Gly Val Leu Leu Phe Ile Gln Leu Val Pro Val Asp Tyr Tyr Phe Leu
221 410                   415                   420                   425
223 tcc att ggt ctg gtc atg ctg gga aaa ttt ggg atc acc tct gct ttc     1469
224 Ser Ile Gly Leu Val Met Leu Gly Lys Phe Gly Ile Thr Ser Ala Phe
225                   430                   435                   440
227 tcc atg ctg tat gtc ttc act gct gag ctc tac cca acc ctg gtc agg     1517
228 Ser Met Leu Tyr Val Phe Thr Ala Glu Leu Tyr Pro Thr Leu Val Arg
229                   445                   450                   455
231 aac atg gcg gtg ggg gtc aca tcc acg gcc tcc aga gtg ggc agc atc     1565
232 Asn Met Ala Val Gly Val Thr Ser Thr Ala Ser Arg Val Gly Ser Ile
233         460                   465                   470
235 att gcc ccc tac ttt gtt tac ctc ggt gct tac aac aga atg ctg ccc     1613
236 Ile Ala Pro Tyr Phe Val Tyr Leu Gly Ala Tyr Asn Arg Met Leu Pro
237         475                   480                   485
239 tac atc gtc atg ggt agt ctg act gtc ctg att gga atc ttc acc ctt     1661
240 Tyr Ile Val Met Gly Ser Leu Thr Val Leu Ile Gly Ile Phe Thr Leu
241 490                   495                   500                   505
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243 ttt ttc cct gaa agt ttg gga atg act ctt cca gaa acc tta gag cag      1709
244 Phe Phe Pro Glu Ser Leu Gly Met Thr Leu Pro Glu Thr Leu Glu Gln
245             510                   515                   520
247 atg cag aaa gtg aaa tgg ttc aga tct ggg aaa aaa aca aga gac tca      1757
248 Met Gln Lys Val Lys Trp Phe Arg Ser Gly Lys Lys Thr Arg Asp Ser
249             525                   530                   535
251 atg gag aca gaa gaa aat ccc aag gtt cta ata act gca ttc              1799
252 Met Glu Thr Glu Glu Asn Pro Lys Val Leu Ile Thr Ala Phe
253         540                   545                   550
255 tgaaaaaata tctaccccat ttggtgaagt gaaaaacaga aaaataagac cctgtggaga    1859
257 aattcgttgt tcccactgaa atggactgac tgtaacgatt gacaccaaaa tgaaccttgc    1919
259 tatcaagaaa tgctcgtcat acagtaaact ctggatgatt cttccagata atgtccttgc    1979
261 tttacaaacc aaccatttct agagagtctc cttactcatt aattcaatga aatggattgg    2039
263 taagatgtct tgaaaacatg ttagtcaagg actggtaaaa tacatataaa gattaacact    2099
265 catttccaat catacaaata ctatccaaat aaaaat                              2135
267 <210> SEQ ID NO: 3
268 <211> LENGTH: 557
269 <212> TYPE: PRT
270 <213> ORGANISM: Homo sapiens
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277             20                  25                  30
279 Asn Gly Phe Thr Gly Leu Ser Ser Val Phe Leu Ile Ala Thr Pro Glu
280             35                  40                  45
282 His Arg Cys Arg Val Pro Asp Ala Ala Asn Leu Ser Ser Ala Trp Arg
283         50                  55                  60
285 Asn His Thr Val Pro Leu Arg Leu Arg Asp Gly Arg Glu Val Pro His
286     65                  70                  75
288 Ser Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Ala Leu
289 80                  85                  90                  95
291 Gly Leu Glu Pro Gly Arg Asp Val Asp Leu Gly Gln Leu Glu Gln Glu
292             100                 105                 110
294 Ser Cys Leu Asp Gly Trp Glu Phe Ser Gln Asp Val Tyr Leu Ser Thr
295             115                 120                 125
297 Ile Val Thr Glu Trp Asn Leu Val Cys Glu Asp Asp Trp Lys Ala Pro
298         130                 135                 140
300 Leu Thr Ile Ser Leu Phe Phe Val Gly Val Leu Leu Gly Ser Phe Ile
301     145                 150                 155
303 Ser Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Asn Val Leu Phe Val
304 160                 165                 170                 175
306 Thr Met Gly Met Gln Thr Gly Phe Ser Phe Leu Gln Ile Phe Ser Lys
307             180                 185                 190
309 Asn Phe Glu Met Phe Val Val Leu Phe Val Leu Val Gly Met Gly Gln
310             195                 200                 205
312 Ile Ser Asn Tyr Val Ala Ala Phe Val Leu Gly Thr Glu Ile Leu Gly
313         210                 215                 220
315 Lys Ser Val Arg Ile Ile Phe Ser Thr Leu Gly Val Cys Ile Phe Tyr
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VERIFICATION SUMMARY   DATE: 08/07/2001
PATENT APPLICATION: **US/09/521,195**   TIME: 13:22:28

Input Set : **A:\06501-057001.txt**
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